

## Sequence Listing

<110> Kaneka Corporation

<120> Method of inducing gene expression in plant and plant treated thereby

<130> T619. PBT-2

<150> JP2000-180466

<151> 2000-06-15

<160> 11

<210> 1

<211> 699

<212> DNA

<213> *Streptomyces virginiae*

<220>

<221> CDS

<222> (1) ... (699)

<300>

<301> Okamoto, S., Nakamura, K., Nihira, T. and Yamada, Y.

<302> Virginiae butanolide binding protein from *Streptomyces virginiae*. Evidence that VbrA is not the virginiae butanolide binding protein and reidentification of the true binding protein

<303> The Journal of Biological Chemistry

<304> 270

<305> 20

<306> 12319-12326

<307> 1995-05-19

<308> D32251

<309> 1994-07-19

<400> 1

atg gca gtg cga cac gaa cgg gtg gca gtg cga cag gaa cgg gcc gtc 48

Met	Ala	Val	Arg	His	Glu	Arg	Val	Ala	Val	Arg	Gln	Glu	Arg	Ala	Val	
1				5					10					15		
cgc	acg	cgg	cag	gcg	atc	gtg	cgg	gca	gcc	gcc	tcg	gtc	ttc	gac	gag	96
Arg	Thr	Arg	Gln	Ala	Ile	Val	Arg	Ala	Ala	Ala	Ser	Val	Phe	Asp	Glu	
			20					25					30			
tac	ggg	ttc	gag	gcc	gcc	aca	gtg	gca	gag	atc	ctc	tcg	cgg	gcc	tcg	144
Tyr	Gly	Phe	Glu	Ala	Ala	Thr	Val	Ala	Glu	Ile	Leu	Ser	Arg	Ala	Ser	
			35					40					45			
gtc	acc	aag	ggc	gcg	atg	tac	ttc	cac	ttc	gct	tcc	aag	gaa	gag	ctg	192
Val	Thr	Lys	Gly	Ala	Met	Tyr	Phe	His	Phe	Ala	Ser	Lys	Glu	Glu	Leu	
			50				55					60				
gcc	cgc	ggc	gtg	ctg	gcc	gag	cag	acc	ctg	cac	gtg	gcg	gtg	ccg	gaa	240
Ala	Arg	Gly	Val	Leu	Ala	Glu	Gln	Thr	Leu	His	Val	Ala	Val	Pro	Glu	
65				70					75					80		
tcc	ggc	tcc	aag	gcg	cag	gaa	ctg	gta	gac	ctc	acc	atg	ctg	gtc	gcc	288
Ser	Gly	Ser	Lys	Ala	Gln	Glu	Leu	Val	Asp	Leu	Thr	Met	Leu	Val	Ala	
				85					90					95		
cac	ggc	atg	ctg	cac	gat	ccg	atc	ctg	cgg	gcg	ggc	acg	cgg	ctc	gca	336
His	Gly	Met	Leu	His	Asp	Pro	Ile	Leu	Arg	Ala	Gly	Thr	Arg	Leu	Ala	
			100					105					110			
ctg	gac	cag	ggg	gcg	gtg	gac	ttc	tcc	gac	gcc	aac	ccg	ttc	ggc	gag	384
Leu	Asp	Gln	Gly	Ala	Val	Asp	Phe	Ser	Asp	Ala	Asn	Pro	Phe	Gly	Glu	
			115					120					125			
tgg	ggc	gac	atc	tgc	gcc	cag	ctc	ctg	gcg	gag	gca	cag	gaa	cgg	ggg	432
Trp	Gly	Asp	Ile	Cys	Ala	Gln	Leu	Leu	Ala	Glu	Ala	Gln	Glu	Arg	Gly	
			130				135					140				
gag	gtg	ctt	ccg	cac	gtg	aac	ccg	aaa	aag	acc	ggc	gac	ttc	atc	gtc	480
Glu	Val	Leu	Pro	His	Val	Asn	Pro	Lys	Lys	Thr	Gly	Asp	Phe	Ile	Val	
145					150					155					160	

ggc tgc ttc acc ggg ctc cag gcg gtc tcc cgg gtc acc tcc gac cgc 528  
 Gly Cys Phe Thr Gly Leu Gln Ala Val Ser Arg Val Thr Ser Asp Arg  
                   165                  170                  175

cag gac ctc ggc cac cgg atc tcg gtg atg tgg aac cac gtg ctg ccc 576  
 Gln Asp Leu Gly His Arg Ile Ser Val Met Trp Asn His Val Leu Pro  
                   180                  185                  190

agc atc gtg ccg gcg tcc atg ctg acc tgg atc gaa acc ggc gag gag 624  
 Ser Ile Val Pro Ala Ser Met Leu Thr Trp Ile Glu Thr Gly Glu Glu  
                   195                  200                  205

cgg atc ggg aag gtc gcg gcg gcg gcc gag gcc gcc gag gct gcg gag 672  
 Arg Ile Gly Lys Val Ala Ala Ala Ala Glu Ala Ala Glu Ala Ala Glu  
                   210                  215                  220

gcc tcc gag gcc gcc tcc gac gag tag 699  
 Ala Ser Glu Ala Ala Ser Asp Glu  
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<210> 2

<211> 232

<212> PRT

<213> *Streptomyces virginiae*

<400> 2

Met Ala Val Arg His Glu Arg Val Ala Val Arg Gln Glu Arg Ala Val  
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Arg Thr Arg Gln Ala Ile Val Arg Ala Ala Ala Ser Val Phe Asp Glu  
                   20                  25                  30

Tyr Gly Phe Glu Ala Ala Thr Val Ala Glu Ile Leu Ser Arg Ala Ser  
                   35                  40                  45

Val Thr Lys Gly Ala Met Tyr Phe His Phe Ala Ser Lys Glu Glu Leu  
                   50                  55                  60

Ala Arg Gly Val Leu Ala Glu Gln Thr Leu His Val Ala Val Pro Glu  
65 70 75 80

Ser Gly Ser Lys Ala Gln Glu Leu Val Asp Leu Thr Met Leu Val Ala  
85 90 95

His Gly Met Leu His Asp Pro Ile Leu Arg Ala Gly Thr Arg Leu Ala  
100 105 110

Leu Asp Gln Gly Ala Val Asp Phe Ser Asp Ala Asn Pro Phe Gly Glu  
115 120 125

Trp Gly Asp Ile Cys Ala Gln Leu Leu Ala Glu Ala Gln Glu Arg Gly  
130 135 140

Glu Val Leu Pro His Val Asn Pro Lys Lys Thr Gly Asp Phe Ile Val  
145 150 155 160

Gly Cys Phe Thr Gly Leu Gln Ala Val Ser Arg Val Thr Ser Asp Arg  
165 170 175

Gln Asp Leu Gly His Arg Ile Ser Val Met Trp Asn His Val Leu Pro  
180 185 190

Ser Ile Val Pro Ala Ser Met Leu Thr Trp Ile Glu Thr Gly Glu Glu  
195 200 205

Arg Ile Gly Lys Val Ala Ala Ala Ala Glu Ala Ala Glu Ala Ala Glu  
210 215 220

Ala Ser Glu Ala Ala Ser Asp Glu  
225 230 235

<210> 3

<211> 26

<212> DNA

<213> *Streptomyces virginiae*

<300>

<301> Kinoshita, H., Tsuji, T., Ipposhi, H., Nihira, T. and Yamada, Y.

<302> Characterization of Binding Sequences for Butyrolactone Autoregulator  
Receptors in Streptomyces

<303> Journal of Bacteriology

<304> 181

<305> 16

<306> 5075-5080

<307> 1999-08

<308> D32251

<309> 1994-07-19

<400> 3

agatacatac caaccggttc ttttga 26

<210> 4

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed sequence of the CaMV 35S promoter modified to contain the operator  
BARE-3 element just downstream of its TATA-box

<400> 4

gatattcca ctgacgtaag ggatgacgca caatcccaact atccttcgca agacccttcc 60

tctatataag agatacatac caaccggttc ttttgacggg ggactctaga 110

<210> 5

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed sequence of the CaMV 35S promoter modified to contain the operator  
BARE-3 element just upstream of its TATA-box

<400> 5

gatatctcca ctgacgtaag ggatgacgca caatcagata cataccaacc ggttcttttg 60

actatataag gaagttcatt tcatttggag agaacacggg ggactctaga 110

<210> 6

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed sequence of the CaMV 35S promoter modified to contain the operator BARE-3 elements just downstream and upstream of its TATA-box

<400> 6

gatatctcca ctgacgtaag ggatgacgca caatcagata cataccaacc ggttcttttg 60

actatataag agatacatac caaccggttc ttttgacggg ggactctaga 110

<210> 7

<211> 136

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed sequence of the CaMV 35S promoter modified to contain three of the operator BARE-3 elements just downstream and upstream of its TATA-box

<400> 7

gatatctcca ctgacgtaag ggatgacgca caatcagata cataccaacc ggttcttttg 60

actatataag agatacatac caaccggttc ttttgaagat acataccaac cggttctttt 120

gacgggggac tctaga 136

<210> 8

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed sequence of a backward primer containing the restriction enzyme BamH I recognition sequence for PCR amplification of the barA gene coding region to be cloned by cut with the enzyme

<400> 8

taggatccat aaatggcagt gcgacac 27

<210> 9

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed sequence of a forward primer containing the restriction enzyme Sac I recognition sequence for PCR amplification of the barA gene coding region to be cloned by cut with the enzyme

<400> 9

tagagtcct actcgtcgga ggcggcc 27

<210> 10

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed sequence of one of paired oligo DNAs for construction of the modified CaMV 35S promoter containing three of the operator BARE-3 elements just downstream and upstream of its TATA-box

<400> 10

cggatatctc cactgacgta agggatgacg cacaatcaga tacataccaa ccggttcttt 60

tgactat 67

<210> 11

<211> 89

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed sequence of the other of paired oligo DNAs for construction of the modified CaMV 35S promoter containing three of the operator BARE-3 elements just downstream and upstream of its TATA-box

<400> 11

gctctagagt ccccgctcaa aagaaccggt tggtatgtat cttcaaaaga accggttggt 60

atgtatctct tatatagtca aaagaaccg 89